D.FOX

1600

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,817A

DATE: 10/05/2001
TIME: 13:55:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\10052001\I674817A.raw

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    3 <110> APPLICANT: Lorz, et al.
    5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM
WHEAT AND
    6        WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH
    8 <130> FILE REFERENCE: 514413-3849
   10 <140> CURRENT APPLICATION NUMBER: 09/674,817A
C--> 11 <141> CURRENT FILING DATE: 2001-11-06
   13 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03141
   14 <151> PRIOR FILING DATE: 1999-05-07
   16 <150> PRIOR APPLICATION NUMBER: 19820608.9
   17 <151> PRIOR FILING DATE: 1998-05-08
   19 <160> NUMBER OF SEQ ID NOS: 10
   21 <170> SOFTWARE: PatentIn version 3.0
   23 <210> SEQ ID NO: 1
   24 <211> LENGTH: 2997
   25 <212> TYPE: DNA
   26 <213> ORGANISM: Triticum aestivum L. cv. Florida
   28 <220> FEATURE:
   29 <221> NAME/KEY: CDS
   30 <222> LOCATION: (3)..(296)
   31 <223> OTHER INFORMATION: exon 1
   34 <220> FEATURE:
   35 <221> NAME/KEY: CDS
   36 <222> LOCATION: (2145)..(2921)
   37 <223> OTHER INFORMATION: exon 3
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   41 <221> NAME/KEY: Intron
   42 <222> LOCATION: (297)..(396)
   43 <223> OTHER INFORMATION: intron 1
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   47 <221> NAME/KEY: CDS
   48 <222> LOCATION: (397)..(1617)
   49 <223> OTHER INFORMATION: exon 2
   52 <220> FEATURE:
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   54 <222> LOCATION: (1618)..(2144)
   55 <223> OTHER INFORMATION: intron 2
   58 <400> SEQUENCE: 1
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   60    Ser Gly Pro Ala Pro Arg Leu Arg Arg Trp Arg Pro Asn Ala Thr
   61    1               5                   10                  15
   63 gcg ggg aag ggg gtc ggc gag gtg tgc gcc gcg gtt gtc gag gcg gcg        95
   64 Ala Gly Lys Gly Val Gly Glu Val Cys Ala Ala Val Val Glu Ala Ala
   65                  20                  25                  30
   67 acg aag gta gag gac gag ggg gag gag gac gag ccg gtg gcg gag gac       143
   68 Thr Lys Val Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp
   69              35                  40                  45
   71 agg tac gcg ctc ggc ggc gcg tgc agg gtg ctc gcc gga atg ccc gcg       191
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10/5/01

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72 Arg Tyr Ala Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Ala
73         50              55              60            ,
75 ccg ctg ggc gcc acc gcg ctc gcc ggc ggg gtc aat ttc gcc gtc tat    239
76 Pro Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr
77      65              70              75
79 tcc ggc gga gcc acc gcc gcg gcg ctc tgc ctc ttc acg cca gaa gat    287
80 Ser Gly Gly Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp
81 80              85              90                      95
83 ctc aag gcg gtggggttgc ctcccgagta gagttcatca gctttgcgtg           336
84 Leu Lys Ala
87 cgccgcgcgc cccttttttg ggcctgcaat ttaagttttg tactggggca aatgctgcag  396
89 gat agg gtg acc gag gag gtt ccc ctt gac ccc ctg atg aat cgg acc    444
90 Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn Arg Thr
91      100             105             110
93 ggg aac gtg tgg cat gtc ttc atc gaa ggc gag ctg cac aac atg ctt    492
94 Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn Met Leu
95 115             120             125             130
97 tac ggg tac agg ttc gac ggc acc ttt gct cct cac tgc ggg cac tac    540
98 Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly His Tyr
99              135             140             145
101 ctt gat gtt tcc aat gtc gtg gtg gat cct tat gct aag gca gtg ata   588
102 Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala Val Ile
103             150             155             160
105 agc cga ggg gag tat ggt gtt cca gcg cgt ggt aac aat tgc tgg cct   636
106 Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys Trp Pro
107         165             170             175
109 cag atg gct ggc atg atc cct ctt cca tat agc acg ttt gat tgg gaa   684
110 Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp Trp Glu
111      180             185             190
113 ggc gac cta cct cta aga tat cct caa aag gac ctg gta ata tat gag   732
114 Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile Tyr Glu
115 195             200             205             210
117 atg cac ttg cgt gga ttc acg aag cat gat tca agc aat gta gaa cat   780
118 Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val Glu His
119             215             220             225
121 ccg ggt act ttc att gga gct gtg tcg aag ctt gac tat ttg aag gag   828
122 Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu Lys Glu
123         230             235             240
125 ctt gga gtt aat tgt att gaa tta atg ccc tgc cat gag ttc aac gag   876
126 Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe Asn Glu
127         245             250             255
129 ctg gag tac tca acc tct tct tcc aag atg aac ttt tgg gga tat tct   924
130 Leu Glu Tyr Ser Thr Ser Ser Ser Lys Met Asn Phe Trp Gly Tyr Ser
131      260             265             270
133 acc ata aac ttc ttt tca cca atg aca aga tac aca tca ggc ggg ata   972
134 Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly Gly Ile
135 275             280             285             290
137 aaa aac tgt ggg cgt gat gcc ata aat gag ttc aaa act ttt gta aga   1020
138 Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys Thr Phe Val Arg
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Input Set : A:\ES.txt
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139                 295              300              305
141 gag gct cac aaa cgg gga att gag gtg atc ctg gat gtt gtc ttc aac      1068
142 Glu Ala His Lys Arg Gly Ile Glu Val Ile Leu Asp Val Val Phe Asn
143                 310              315              320
145 cat aca gct gag ggt aat gag aat ggt cca ata tta tca ttt aag ggg      1116
146 His Thr Ala Glu Gly Asn Glu Asn Gly Pro Ile Leu Ser Phe Lys Gly
147                 325              330              335
149 gtc gat aat act aca tac tat atg ctt gca ccc aag gga gag ttt tat      1164
150 Val Asp Asn Thr Thr Tyr Tyr Met Leu Ala Pro Lys Gly Glu Phe Tyr
151         340              345              350
153 aac tat tct ggc tgt ggg aat acc ttc aac tgt aat cat cct gtg gtt      1212
154 Asn Tyr Ser Gly Cys Gly Asn Thr Phe Asn Cys Asn His Pro Val Val
155 355                 360              365              370
157 cgt caa ttc att gta gat tgt tta aga tac tgg gtg acg gaa atg cat      1260
158 Arg Gln Phe Ile Val Asp Cys Leu Arg Tyr Trp Val Thr Glu Met His
159                 375              380              385
161 gtt gat ggt ttt cgt ttt gat ctt gca tcc ata atg acc aga ggt tcc      1308
162 Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Ile Met Thr Arg Gly Ser
163                 390              395              400
165 agt ctg tgg gat cca gtt aac gtg tat gga gct cca ata gaa ggt gac      1356
166 Ser Leu Trp Asp Pro Val Asn Val Tyr Gly Ala Pro Ile Glu Gly Asp
167                 405              410              415
169 atg atc aca aca ggg aca cct ctt gtt act cca cca ctt att gac atg      1404
170 Met Ile Thr Thr Gly Thr Pro Leu Val Thr Pro Pro Leu Ile Asp Met
171         420              425              430
173 atc agc aat gac cca att ctt gga ggc gtc aag ctc att gct gaa gca      1452
174 Ile Ser Asn Asp Pro Ile Leu Gly Gly Val Lys Leu Ile Ala Glu Ala
175 435                 440              445              450
177 tgg gat gca gga ggc ctc tat caa gta ggt caa ttc cct cac tgg aat      1500
178 Trp Asp Ala Gly Gly Leu Tyr Gln Val Gly Gln Phe Pro His Trp Asn
179                 455              460              465
181 gtt tgg tct gag tgg aat ggg aag tac cgg gac att gtg cgt caa ttc      1548
182 Val Trp Ser Glu Trp Asn Gly Lys Tyr Arg Asp Ile Val Arg Gln Phe
183         470              475              480
185 att aaa ggc act gat gga ttt gct ggt ggt ttt gcc gaa tgt ctt tgt      1596
186 Ile Lys Gly Thr Asp Gly Phe Ala Gly Gly Phe Ala Glu Cys Leu Cys
187         485              490              495
189 gga agt cca cac cta tac cag gtaagttgtg gcaatacttg taaatgagtt      1647
190 Gly Ser Pro His Leu Tyr Gln
191         500              505
193 gagtgaatgt cacctggatt ttttatatat accacatgat gatacacatc taaatatata      1707
195 acaatcatag tgtatgcata tgcatttggc taagaagtat tagtgtatac actagtgcta      1767
197 tatataggtt ttaacaccca acttgccaat gaaggaacat agggctttct agttatctta      1827
199 tttatttgtc cggtgaataa tccactgaaa aattccagcc atgtcatttt ttaggggggg      1887
201 agaagaaact atattgattt gcccccctaa aagaagccat ctcagaattc ataggtaagt      1947
203 tgcttttctg taaagaaagg aaaacgactt catactttct atcggtgcta acttagctcg      2007
205 atgtatattt gtaagatgaa tgccaaattt aatttgtcgg ataatttgat ctgttattca      2067
207 caaatttcta tttggtttct ctagaaatca aaccagtaac ttgttattgg cactgcaact      2127
209 tcttattgat taatcag gca gga gga agg aaa cct tgg cac agt atc aac      2177
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210                     Ala Gly Gly Arg Lys Pro Trp His Ser Ile Asn
211                                 510                 515
213  ttt gta tgt gca cat gat gga ttt aca ctg gct gat ttg gta aca tat      2225
214  Phe Val Cys Ala His Asp Gly Phe Thr Leu Ala Asp Leu Val Thr Tyr
215          520                 525                 530
217  aat aag aag tac aat tta cca aat ggg gag aac aac aga gat gga gaa      2273
218  Asn Lys Lys Tyr Asn Leu Pro Asn Gly Glu Asn Asn Arg Asp Gly Glu
219          535                 540                 545
221  aat cac aat ctt agc tgg aat tgt ggg gag gaa gga gaa ttc gca aga      2321
222  Asn His Asn Leu Ser Trp Asn Cys Gly Glu Glu Gly Glu Phe Ala Arg
223          550                 555                 560
225  ttg tct gtc aaa aga ttg agg aag agg cag atg cgc aat ttc ttt gtt      2369
226  Leu Ser Val Lys Arg Leu Arg Lys Arg Gln Met Arg Asn Phe Phe Val
227  565                 570                 575                 580
229  tgt ctc atg gtt tct caa gga gtt cca atg ttc tac atg ggt gat gaa      2417
230  Cys Leu Met Val Ser Gln Gly Val Pro Met Phe Tyr Met Gly Asp Glu
231                  585                 590                 595
233  tat ggc cac aca aaa ggg ggc aac aac aat aca tac tgc cat gat tct      2465
234  Tyr Gly His Thr Lys Gly Gly Asn Asn Asn Thr Tyr Cys His Asp Ser
235          600                 605                 610
237  tat gtc aat tat ttt cgc tgg gat aaa aaa gaa caa tac tct gag ttg      2513
238  Tyr Val Asn Tyr Phe Arg Trp Asp Lys Lys Glu Gln Tyr Ser Glu Leu
239          615                 620                 625
241  cac cga ttc tgc tgc ctc atg acc aaa ttc cgc aag gag tgc gag ggt      2561
242  His Arg Phe Cys Cys Leu Met Thr Lys Phe Arg Lys Glu Cys Glu Gly
243          630                 635                 640
245  ctt ggc ctt gag gac ttt cca acg gcc aaa cgg ctg cag tgg cat ggt      2609
246  Leu Gly Leu Glu Asp Phe Pro Thr Ala Lys Arg Leu Gln Trp His Gly
247  645                 650                 655                 660
249  cat cag cct ggg aag cct gat tgg tct gag aat agc cga ttc gtt gcc      2657
250  His Gln Pro Gly Lys Pro Asp Trp Ser Glu Asn Ser Arg Phe Val Ala
251                  665                 670                 675
253  ttt tcc atg aaa gat gaa aga cag ggc gag atc tat gtg gcc ttc aac      2705
254  Phe Ser Met Lys Asp Glu Arg Gln Gly Glu Ile Tyr Val Ala Phe Asn
255          680                 685                 690
257  acc agc cac tta ccg gcc gtt gtt gag ctc cca gag cgc gca ggg cgc      2753
258  Thr Ser His Leu Pro Ala Val Val Glu Leu Pro Glu Arg Ala Gly Arg
259          695                 700                 705
261  cgg tgg gaa ccg gtg gtg gac aca ggc aag cca gca cca tac gac ttc      2801
262  Arg Trp Glu Pro Val Val Asp Thr Gly Lys Pro Ala Pro Tyr Asp Phe
263          710                 715                 720
265  ctc acc gac gac tta cct gat cgc gct ctc acc ata cac cag ttc tcg      2849
266  Leu Thr Asp Asp Leu Pro Asp Arg Ala Leu Thr Ile His Gln Phe Ser
267  725                 730                 735                 740
269  cat ttc ctc tac tcc aac ctc tac ccc atg ctc agc tac tca tcg gtc      2897
270  His Phe Leu Tyr Ser Asn Leu Tyr Pro Met Leu Ser Tyr Ser Ser Val
271                  745                 750                 755
273  atc cta gta ttg cgc cct gat gtt tgagagacca atatatacag taaataatat      2951
274  Ile Leu Val Leu Arg Pro Asp Val
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281 <211> LENGTH: 764
282 <212> TYPE: PRT
283 <213> ORGANISM: Triticum aestivum L. cv. Florida
285 <400> SEQUENCE: 2
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292         20              25              30
295 Lys Val Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp Arg
296         35              40              45
299 Tyr Ala Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Ala Pro
300     50              55              60
303 Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr Ser
304 65              70              75              80
307 Gly Gly Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp Leu
308             85              90              95
311 Lys Ala Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn
312             100             105             110
315 Arg Thr Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn
316         115             120             125
319 Met Leu Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly
320     130             135             140
323 His Tyr Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala
324 145             150             155             160
327 Val Ile Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys
328             165             170             175
331 Trp Pro Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp
332             180             185             190
335 Trp Glu Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile
336         195             200             205
339 Tyr Glu Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val
340     210             215             220
343 Glu His Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu
344 225             230             235             240
347 Lys Glu Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe
348             245             250             255
351 Asn Glu Leu Glu Tyr Ser Thr Ser Ser Lys Met Asn Phe Trp Gly
352             260             265             270
355 Tyr Ser Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly
356         275             280             285
359 Gly Ile Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys Thr Phe
360     290             295             300
363 Val Arg Glu Ala His Lys Arg Gly Ile Glu Val Ile Leu Asp Val Val
364 305             310             315             320
367 Phe Asn His Thr Ala Glu Gly Asn Glu Asn Gly Pro Ile Leu Ser Phe
368             325             330             335
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VERIFICATION SUMMARY   DATE: 10/05/2001
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date